CLAIMS

What is claimed is:

1. A method of changing the phenotype or biochemistry of a plant, comprising:

(a) expressing transiently a nucleic acid sequence from a donor organism selected from the group consisting of *Monera, Protista, Fungi*, and *Animalia*, in a positive sense orientation in a host plant;

(b) determining one or more phenotypic or biochemical changes in said host plant.

2. A method of determining a change in phenotype or biochemistry in a plant due to a cytoplasmic expression of a nucleic acid in a positive sense orientation, comprising:

(a) expressing transiently a nucleic acid sequence from a donor organism selected from the group consisting of *Monera, Protista, Fungi*, and *Animalia*, in a positive sense orientation in a host plant;

(b) determining one or more biochemical or phenotypic changes in said host plant; and

(c) correlating said one or more biochemical or phenotypic changes to a host plant that is uninfected.

3. The method according to Claim 2, further comprises the step of correlating said one or more biochemical or phenotypic changes to a host plant that is infected with a viral vector that contains a known nucleic acid sequence of like size in a positive sense orientation, wherein said known nucleic acid sequence has similar size but is different in sequence from said nucleic acid sequence in (a).

4. A method of determining the presence of a trait in a plant, comprising:

(a) expressing transiently a nucleic acid sequence from a donor organism selected from the group consisting of *Monera, Protista, Fungi*, and *Animalia*, in a positive sense orientation in a host plant;

(b) determining one or more biochemical or phenotypic changes in said host plant;

(c) correlating said one or more biochemical or phenotypic changes to a host plant that is uninfected; and

(d) identifying a trait present in said uninfected host plant.

5. The method according to Claim 4, further comprises the step of correlating said one or more biochemical or phenotypic changes to a host plant that is infected with a viral vector that contains a known nucleic acid sequence in a positive sense orientation, wherein said known nucleic acid sequence has similar size but is different in sequence from said nucleic acid sequence in (a).

6. A method of determining the presence of a trait in a plant, comprising:

(a) expressing transiently nucleic acid sequence from a donor organism selected from the group consisting of *Monera, Protoctista, Fungi*, and *Animalia*, in a positive sense orientation in a host plant;

(b) determining one or more biochemical or, phenotypic changes in said host plant;

(c) correlating said one or more biochemical or phenotypic changes to a host plant that is uninfected; and

(d) identifying a trait present in said infected host plant.

7. The method according to Claim 6, further comprises the step of correlating said one or more biochemical or phenotypic changes to a host plant that is infected with a viral vector that contains a known nucleic acid sequence but in a positive sense orientation, wherein said known nucleic acid sequence has similar size but is different in sequence from said nucleic acid sequence in (a).

8. The method according to Claim 1, 2, 4, or 6, wherein said nuclei acid sequence from said donor has not been identified.

9. The method according to Claim 1, 2, 4, or 6, wherein said host plant is selected from the group consisting of food crops, seed crops, oil crops, ornamental crops and forestry.

10. The method according to Claim 9, wherein said host plant is *Nicotiana*.

11. The method according to Claim 10, wherein said host plant is *Nicotiana benthamina* or *Nicotiana clevlandii*.

12. The method according to Claim 1, 2, 4, or 6, wherein said nucleic acid sequence is derived from a library of cDNAs, genomic DNAs, or a pool of mRNAs, which represents all or part of the donor organism genome.

13. The method according to Claim 12, further comprising the step of cloning said nucleic acid sequence into a plant viral vector.

14. The method according to Claim 13, wherein the plant viral vector genome is capped or uncapped.

15. The method according to Claim 13, further comprising the step of infecting said host plant with a recombinant viral nucleic acid comprising said nucleic acid sequence.

16. The method according to Claim 15, wherein said recombinant viral nucleic acid further comprises a native plant viral subgenomic promoter and a plant viral coat protein coding sequence.

17. The method according to Claim 16, wherein said recombinant viral nucleic acid further comprises a non-native plant viral subgenomic promoter, said native plant viral subgenomic promoter initiates transcription of said plant viral coat protein sequence and said non-native plant viral subgenomic promoter initiates transcription of said nucleic acid sequence.

18. The method according to Claim 13, wherein a plus sense RNA is produced in the cytoplasm of said host plant, and said plus sense RNA results in overexpression of a protein in said host plant.

19. The method according to Claim 13, wherein a plus sense RNA is produced in the cytoplasm of said host plant, and said plus sense RNA results in an enhanced or reduced expression of an endogenous gene in said host plant.

20. The method according to Claim 18 or 19 wherein said nucleic acid sequence encodes a GTP binding protein.

21. The method according to Claim 19, wherein said plus sense RNA results in a reduced expression of an endogenous gene in said host plant.

22. The method according to Claim 21, wherein said nucleic acid sequence does not contain a start codon.

23. The method according to Claim 21, wherein said nucleic acid encodes an untranslated region.

24. The method according to Claim 13, wherein said recombinant viral nucleic acids are derived from a plant virus.

25. The method according to Claim 24, wherein said plant virus is selected from the group consisting of a potyvirus, a tobamovirus, a bromovirus, and a geminivirus.

26. The method according to Claim 25, wherein said potyvirus is a rice necrosis virus.

27. The method according to Claim 1, 2, 4 or 6, wherein said phenotypic changes are changes in growth rates, morphology, or color.

28. A method of determining the presence of a trait in a plant, comprising:

(a) expressing transiently a nucleic acid sequence of a donor organism selected from the group consisting of *Monera, Protista, Fungi*, and *Animalia*, in a positive sense orientation in a host plant;

(b) determining phenotypic or biochemical changes in said host plant; and

(c) correlating said expression with said phenotypic or biochemical changes, wherein said nucleic acid sequence comprising a GTP binding protein open reading frame having a positive sense orientation.

29. The method according to Claim 28, wherein said GTP binding protein is

selected from the group consisting of *rab* family, and ADP-ribosylation factor family.

30. A method for identifying a nucleic acid sequence in a donor organism selected from the group consisting of *Monera, Protista, Fungi*, and *Animalia*, having the same function as that in a host plant, said method comprising the steps of:

(a) preparing a library of cDNAs, genomic DNAs, or a pool of mRNAs of said donor organism,

(b) constructing recombinant viral nucleic acids comprising a nucleic acid insert derived from said library,

(c) infecting each said host plant with one of said recombinant viral nucleic acids, and expressing transiently said nucleic acid in a positive sense orientation in said host plant,

(d) growing said infected host plant,

(e) determining one or more changes in said host plant,

(f) identifying said recombinant viral nucleic acid that results in changes in said host plant, and

(g) determining the sequence of said nucleic acid insert in said recombinant viral nucleic acid, and

(h) determining the sequence of an entire open reading frame of said donor from which said nucleic acid insert is derived.

31. The method according to Claim 30, wherein said donor organism is human.

32. A method for identifying a human nucleic acid sequence, said method comprising the steps of:

(a) preparing a human cDNA library,

(b) constructing recombinant viral nucleic acids comprising a nucleic acid insert derived from said library,

(c) infecting a host plant with one of said recombinant viral nucleic acids, and expressing transiently said nucleic acid in a positive sense orientation in said host plant,

(d) growing said infected host plant,

(e) determining one or more changes in said host plant,

(f) identifying said recombinant viral nucleic acid that results in said changes in said host plant,

(g) determining the sequence of said nucleic acid insert in said recombinant viral nucleic acid, and

(h) determining the sequence of an entire open reading frame in said human from which said nucleic acid insert is derived.

33. A method for isolating human cDNAs, said method comprising the steps of:

(a) obtaining a cDNA library from a human organism,

(b) constructing recombinant viral nucleic acids comprising a nucleic acid insert derived from said library,

(c) infecting a host plant with said recombinant viral nucleic acids, and expressing transiently said nucleic acid in a positive sense orientation in said host plant,

(d) growing said infected host plant,

(e) determining one or more changes in said host plant,

(f) identifying said recombinant viral nucleic acid that results in changes in said host plant,

(g) sequencing and labeling said nucleic acid insert in said recombinant viral nucleic acid of (f),

(h) probing filters or slides containing full-length human cDNAs with said labeled nucleic acid insert, and

(i) isolating said full-length human cDNA that hybridizes to said labeled nucleic acid insert.

34. A method for humanizing a plant cDNA, said method comprising the steps of:

(a) obtaining a cDNA library from a human organism,

(b) constructing recombinant viral nucleic acids comprising a nucleic acid insert derived from said library,

(c) infecting a host plant with said recombinant viral nucleic acids, and expressing transiently said nucleic acid in a positive sense orientation in said host plant,

(d) growing said infected host plant,

(e) determining one or more changes in said host plant,

(f) identifying said recombinant viral nucleic acid that results in changes in said host plant,

(g) sequencing and labeling said nucleic acid insert in said recombinant viral nucleic acid of (f),

(h) probing filters or slides containing full-length human cDNAs or full-length plant cDNAs with said labeled nucleic acid insert,

(i) isolating said full-length human cDNA and plant cDNA that hybridize to said labeled nucleic acid insert,

(j) comparing the amino acid sequences derived from said human cDNA and said plant cDNA, and

(k) changing said plant cDNA sequence so that it encodes the same amino acid sequence as said human cDNA encodes.

35. The method according to Claim 32, 33, or 34 wherein said nucleic acid sequence encodes a protein that regulates growth of cells or organisms in human.

36. The method according to Claim 35, wherein said protein is a L19 ribosomal protein, a GTP binding protein, or a S18 ribosomal protein.

37. The method according to Claim 32, 33, or 34 wherein said nucleic acid sequence encodes a protein that regulates a development fate in human.

38. The method according to Claim 37, wherein said protein belongs to a rhodopsin family.

39. A method of increasing yield of a grain crop, said method comprising expressing transiently a nucleic acid sequence of a non-plant organism in a positive sense orientation in said grain crop, wherein said expressing results in stunted growth and increased seed production of said grain crop.

40. The method according to Claim 39, further comprising the step of cloning said nucleic acid sequence into a plant viral vector.

41. The method according to Claim 40, further comprising infecting said grain crop with a recombinant viral nucleic acid comprising said nucleic acid sequence.

42. The method according to Claim 41, wherein said nucleic acid comprises a GTP binding protein open reading frame having a positive sense orientation.

43. The method according to Claim 39, wherein said grain crop is rice.

44. The method according to Claim 40, wherein said plant viral vector is derived from a virus selected from the group consisting of a Brome Mosaic virus, a Rice Necrosis virus, and a geminivirus.

45. A method of compiling a positive sense functional gene profile of an organism comprising:

(a) preparing a vector library of DNA or RNA sequences from a donor organism, each sequence being in a positive sense orientation;

(b) infecting a plant host with a vector;

(c) transiently expressing the donor DNA or RNA sequence in said growing plant host;

(d) determining one or more phenotypic or biochemical changes in said plant host;

(e) identifying an associated trait where a phenotypic or biochemical change occurs;

(f) identifying a donor gene associated with the trait;

(g) identifying a plant host gene, which is associated with the trait; and

repeating steps b) – g) until a positive sense functional gene profile of said plant host and/or of said donor organism is compiled.